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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/088,961

DATE: 04/10/2003
TIME: 11:22:04

Input Set : A:\-48-1.app
Output Set: N:\CRF4\04102003\J088961.raw

3 <110> APPLICANT: Luo, Ying
4 Xu, Xiang
5 Rigel Pharmaceuticals, Inc.
7 <120> TITLE OF INVENTION: Novel TRAF4 Associated Cell Cycle Proteins,
8 Compositions and Methods of Use
10 <130> FILE REFERENCE: 021044-004810US
12 <140> CURRENT APPLICATION NUMBER: US 10/088,961
C--> 13 <141> CURRENT FILING DATE: 2002-12-30
15 <150> PRIOR APPLICATION NUMBER: US 09/404,010
16 <151> PRIOR FILING DATE: 1999-09-23
18 <150> PRIOR APPLICATION NUMBER: WO PCT/US00/40987
19 <151> PRIOR FILING DATE: 2000-09-25
21 <160> NUMBER OF SEQ ID NOS: 17
23 <170> SOFTWARE: PatentIn Ver. 2.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 2644
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (43)..(2472)
33 <223> OTHER INFORMATION: cell cycle protein Mkinase
35 <400> SEQUENCE: 1
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38 gggccctggg ccctgcaccg cggccgcaag aaggccacag gcagccccgt gtccatcttc 180
39 gtctatgatg tgaagcctgg cgcggaarga gcagaccag gtggccaaag ctgccttcaa 240
40 gcrgettcaa aactctacgg caccccaaca tcrctggctt acatcgatgg actggagaca 300
41 gaaaaaatgcc tccacgtcgt gacagaggct gtgaccccg tgggaatata cctcaaggcg 360
42 agagtggagg ctggtggcct gaaggagctg gagatctcct gggggctaca ccagatcgtg 420
43 aaagccctca gttcctggt caacgactgc agcctcatcc acaacaatgt ctgcatggcc 480
44 gccgtgttcg tggaccgagc tggcgagtg aagcttggg gcctggacta catgtattcg 540
45 gccagaggca acggtggggg acctccccgc aaggggatcc ccgagcttga gcagtatgac 600
46 ccccgaggag tggctgacag cagtggcaga gtggtcagag agaagtggc agcagacatg 660
47 tggcgcttgg gctgcctcat ttgggaagtc ttcaatgggc ccctacctcg ggcagcagcc 720
48 ctacgcaacc ctgggaagat ccccaaaacg ctggcgcccc attactgtga gctggtggga 780
49 gcaaacccca aggtgcgtcc caaccagcc cgcttctcgc agaactgcc ggcacctggt 840
50 ggcttcatga gcaaccgctt tgtagaaacc aacctcttcc tggaggagat tcagatcaaa 900
51 gagccagccg agaagcaaaa attcttccag gagctgagca agagcctgga cgcattccct 960
52 gaggatttct gtcggcaciaa gctgctgccc cagctgctga ccgccttcga gttcggcaat 1020
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54 tatcagcaga agatcatccc tgtggtggtc aagatgttct catccactga ccgggccatg 1140
55 cgcacccgcc tcctgcagca gatggagcag ttcattcagt accttgacga gccaacagtc 1200

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56 aacacccaga tcttccccca cgtcgtacat ggcttcctgg acaccaaccc tgccatccgg 1260
57 gaggagacgg tcaagtccat gctgctcctg gcccacaaagc tgaacgaggc caacctcaat 1320
58 gtggagctga tgaagcactt tgcacggcta caggccaagg atgaacaggg ccccatccgc 1380
59 tgcaacacca cagtctgcct gggcaaaatc ggctcctacc tcagtgtag caccagacac 1440
60 agggtcctta cctctgcctt cagccgagcc actagggacc cgtttgcacc gtcccgggtt 1500
61 ggggtgttcc tgggctttgc tgccacccac aacctctact caatgaacga ctgtgcccag 1560
62 aagatcctgc ctgtgctctg cggctctact gtagatcctg agaaatccgt gcgagaccag 1620
63 gccttcaagg catttcggag ctctctgtcc aaattggagt ctgtgtcgga ggacccgacc 1680
64 cagctggagg aagtggagaa ggatgtccat gcagcctcca gccctggcat gggaggagcc 1740
65 gcagctagct gggcaggctg ggccgtgacc ggggtctcct cactcacctc caagctgac 1800
66 cgttcgcacc caaccactgc cccaacagaa accaacattc cccaaagacc cagcctgaa 1860
67 ggagttcctg ccccagcccc caccctgtt cctgccaccc ctacaacctc aggccactgg 1920
68 gagacgcagg aggaggacaa ggacacagca gaggacagca gcactgctga cagatgggac 1980
69 gacgaagact ggggcagcct ggagcaggag gccaggtctg tgctggccca gcaggacgac 2040
70 tggagcaccg ggggccaagt gagccgtgct agtcagggtc gcaactccga ccacaaatcc 2100
71 tccaaatccc cagagtccga ctggagcagc tgggaagctg agggctcctg ggaacagggc 2160
72 tggcaggagc caagctccca ggagccacct tctgacggta cagggtggc cagcgagtat 2220
73 aactggggtg gccagagtc cagcgacaag ggcqacccct tcgtacctc gtctgcacgt 2280
74 cccagcaccc agccgaggcc agactcttgg ggtgaggaca actgggaggg cctcgagact 2340
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77 aagctggact gaaccgtggc ggtggccctt cccggctgcg gagagcccgc cccacagatg 2520
78 tatttattgt acaaacatg tgagcccggc cggcccagcc aggccatctc acgtgtacat 2580
79 aatcagagcc acaataaatt ctatttcaca aaaaaaaaaa aaaaaaaaaa aaaaaaacct 2640
80 cgag

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83 <210> SEQ ID NO: 2

84 <211> LENGTH: 831

85 <212> TYPE: PRT

86 <213> ORGANISM: Homo sapiens

88 <220> FEATURE:

89 <223> OTHER INFORMATION: amino acid sequence which includes

90 cell cycle protein Mkinase

92 <400> SEQUENCE: 2

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94   1           5           10           15
96 Pro Ala Ala Ala Val Gly Thr Met Trp Phe Phe Ala Arg Asp Pro Val
97           20           25           30
99 Arg Asp Phe Pro Phe Glu Leu Ile Pro Glu Pro Pro Glu Gly Gly Leu
100           35           40           45
102 Pro Gly Pro Trp Ala Leu His Arg Gly Arg Lys Lys Ala Thr Gly Ser
103           50           55           60
105 Pro Val Ser Ile Phe Val Tyr Asp Val Lys Pro Gly Ala Glu Glu Gln
106 65           70           75           80
108 Thr Gln Val Ala Lys Ala Ala Phe Lys Arg Phe Lys Thr Leu Arg His
109           85           90           95
111 Pro Asn Ile Leu Ala Tyr Ile Asp Gly Leu Glu Thr Glu Lys Cys Leu
112           100          105          110
114 His Val Val Thr Glu Ala Val Thr Pro Leu Gly Ile Tyr Leu Lys Ala
115           115          120          125

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117 Arg Val Glu Ala Gly Gly Leu Lys Glu Leu Glu Ile Ser Trp Gly Leu
118      130                      135                      140
120 His Gln Ile Val Lys Ala Leu Ser Phe Leu Val Asn Asp Cys Ser Leu
121 145                      150                      155                      160
123 Ile His Asn Asn Val Cys Met Ala Ala Val Phe Val Asp Arg Ala Gly
124                      165                      170                      175
126 Glu Trp Lys Leu Gly Gly Leu Asp Tyr Met Tyr Ser Ala Gln Gly Asn
127                      180                      185                      190
129 Gly Gly Gly Pro Pro Arg Lys Gly Ile Pro Glu Leu Glu Gln Tyr Asp
130                      195                      200                      205
132 Pro Pro Glu Leu Ala Asp Ser Ser Gly Arg Val Val Arg Glu Lys Trp
133      210                      215                      220
135 Ser Ala Asp Met Trp Arg Leu Gly Cys Leu Ile Trp Glu Val Phe Asn
136 225                      230                      235                      240
138 Gly Pro Leu Pro Arg Ala Ala Ala Leu Arg Asn Pro Gly Lys Ile Pro
139                      245                      250                      255
141 Lys Thr Leu Ala Pro His Tyr Cys Glu Leu Val Gly Ala Asn Pro Lys
142                      260                      265                      270
144 Val Arg Pro Asn Pro Ala Arg Phe Leu Gln Asn Cys Arg Ala Pro Gly
145      275                      280                      285
147 Gly Phe Met Ser Asn Arg Phe Val Glu Thr Asn Leu Phe Leu Glu Glu
148      290                      295                      300
150 Ile Gln Ile Lys Glu Pro Ala Glu Lys Gln Lys Phe Phe Gln Glu Leu
151 305                      310                      315                      320
153 Ser Lys Ser Leu Asp Ala Phe Pro Glu Asp Phe Cys Arg His Lys Leu
154                      325                      330                      335
156 Leu Pro Gln Leu Leu Thr Ala Phe Glu Phe Gly Asn Ala Gly Ala Val
157                      340                      345                      350
159 Val Leu Thr Pro Leu Phe Lys Val Gly Lys Phe Leu Ser Ala Glu Glu
160      355                      360                      365
162 Tyr Gln Gln Lys Ile Ile Pro Val Val Val Lys Met Phe Ser Ser Thr
163      370                      375                      380
165 Asp Arg Ala Met Arg Ile Arg Leu Leu Gln Gln Met Glu Gln Phe Ile
166 385                      390                      395                      400
168 Gln Tyr Leu Asp Glu Pro Thr Val Asn Thr Gln Ile Phe Pro His Val
169                      405                      410                      415
171 Val His Gly Phe Leu Asp Thr Asn Pro Ala Ile Arg Glu Gln Thr Val
172                      420                      425                      430
174 Lys Ser Met Leu Leu Leu Ala Pro Lys Leu Asn Glu Ala Asn Leu Asn
175                      435                      440                      445
177 Val Glu Leu Met Lys His Phe Ala Arg Leu Gln Ala Lys Asp Glu Gln
178      450                      455                      460
180 Gly Pro Ile Arg Cys Asn Thr Thr Val Cys Leu Gly Lys Ile Gly Ser
181 465                      470                      475                      480
183 Tyr Leu Ser Ala Ser Thr Arg His Arg Val Leu Thr Ser Ala Phe Ser
184                      485                      490                      495
186 Arg Ala Thr Arg Asp Pro Phe Ala Pro Ser Arg Val Ala Gly Val Leu
187      500                      505                      510
189 Gly Phe Ala Ala Thr His Asn Leu Tyr Ser Met Asn Asp Cys Ala Gln

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190          515          520          525
192 Lys Ile Leu Pro Val Leu Cys Gly Leu Thr Val Asp Pro Glu Lys Ser
193          530          535          540
195 Val Arg Asp Gln Ala Phe Lys Ala Phe Arg Ser Phe Leu Ser Lys Leu
196 545          550          555          560
198 Glu Ser Val Ser Glu Asp Pro Thr Gln Leu Glu Glu Val Glu Lys Asp
199          565          570          575
201 Val His Ala Ala Ser Ser Pro Gly Met Gly Gly Ala Ala Ala Ser Trp
202          580          585          590
204 Ala Gly Trp Ala Val Thr Gly Val Ser Ser Leu Thr Ser Lys Leu Ile
205          595          600          605
207 Arg Ser His Pro Thr Thr Ala Pro Thr Glu Thr Asn Ile Pro Gln Arg
208          610          615          620
210 Pro Thr Pro Glu Gly Val Pro Ala Pro Ala Pro Thr Pro Val Pro Ala
211 625          630          635          640
213 Thr Pro Thr Thr Ser Gly His Trp Glu Thr Gln Glu Glu Asp Lys Asp
214          645          650          655
216 Thr Ala Glu Asp Ser Ser Thr Ala Asp Arg Trp Asp Asp Glu Asp Trp
217          660          665          670
219 Gly Ser Leu Glu Gln Glu Ala Glu Ser Val Leu Ala Gln Gln Asp Asp
220          675          680          685
222 Trp Ser Thr Gly Gly Gln Val Ser Arg Ala Ser Gln Val Ser Asn Ser
223          690          695          700
225 Asp His Lys Ser Ser Lys Ser Pro Glu Ser Asp Trp Ser Ser Trp Glu
226 705          710          715          720
228 Ala Glu Gly Ser Trp Glu Gln Gly Trp Gln Glu Pro Ser Ser Gln Glu
229          725          730          735
231 Pro Pro Ser Asp Gly Thr Arg Leu Ala Ser Glu Tyr Asn Trp Gly Gly
232          740          745          750
234 Pro Glu Ser Ser Asp Lys Gly Asp Pro Phe Ala Thr Leu Ser Ala Arg
235          755          760          765
237 Pro Ser Thr Gln Pro Arg Pro Asp Ser Trp Gly Glu Asp Asn Trp Glu
238          770          775          780
240 Gly Leu Glu Thr Asp Ser Arg Gln Val Lys Ala Glu Leu Ala Arg Lys
241 785          790          795          800
243 Lys Arg Glu Glu Arg Arg Arg Glu Met Glu Ala Lys Arg Ala Glu Arg
244          805          810          815
246 Lys Val Ala Lys Gly Pro Met Lys Leu Gly Ala Arg Lys Leu Asp
247          820          825          830
250 <210> SEQ ID NO: 3
251 <211> LENGTH: 9
252 <212> TYPE: PRT
253 <213> ORGANISM: Artificial Sequence
255 <220> FEATURE:
256 <223> OTHER INFORMATION: Description of Artificial Sequence:cyclin A
257      destruction box
259 <400> SEQUENCE: 3
260 Arg Thr Val Leu Gly Val Ile Gly Asp
261 1          5

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Input Set : A:\-48-1.app

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264 <210> SEQ ID NO: 4
265 <211> LENGTH: 9
266 <212> TYPE: PRT
267 <213> ORGANISM: Artificial Sequence
269 <220> FEATURE:
270 <223> OTHER INFORMATION: Description of Artificial Sequence:cyclin B1
271     destruction box
273 <400> SEQUENCE: 4
274 Arg Thr Ala Leu Gly Asp Ile Gly Asn
275   1           5
278 <210> SEQ ID NO: 5
279 <211> LENGTH: 27
280 <212> TYPE: PRT
281 <213> ORGANISM: Artificial Sequence
283 <220> FEATURE:
284 <223> OTHER INFORMATION: Description of Artificial Sequence:rat cyclin B
285     destruction box
287 <400> SEQUENCE: 5
288 Tyr Met Thr Val Ser Ile Ile Asp Arg Phe Met Gln Asp Ser Cys Val
289   1           5           10           15
291 Pro Lys Lys Met Leu Gln Leu Val Gly Val Thr
292           20           25
295 <210> SEQ ID NO: 6
296 <211> LENGTH: 28
297 <212> TYPE: PRT
298 <213> ORGANISM: Artificial Sequence
300 <220> FEATURE:
301 <223> OTHER INFORMATION: Description of Artificial Sequence:mouse cyclin B
302     destruction box
304 <400> SEQUENCE: 6
305 Lys Phe Arg Leu Leu Gln Glu Thr Met Tyr Met Thr Val Ser Ile Ile
306   1           5           10           15
308 Asp Arg Phe Met Gln Asn Ser Cys Val Pro Lys Lys
309           20           25
312 <210> SEQ ID NO: 7
313 <211> LENGTH: 27
314 <212> TYPE: PRT
315 <213> ORGANISM: Artificial Sequence
317 <220> FEATURE:
318 <223> OTHER INFORMATION: Description of Artificial Sequence:mouse cyclin B1
319     destruction box
321 <400> SEQUENCE: 7
322 Arg Ala Ile Leu Ile Asp Trp Leu Ile Gln Val Gln Met Lys Phe Arg
323   1           5           10           15
325 Leu Leu Gln Glu Thr Met Tyr Met Thr Val Ser
326           20           25
329 <210> SEQ ID NO: 8
330 <211> LENGTH: 27
331 <212> TYPE: PRT

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/088,961

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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date